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U.S. DEPARTMENT OF COMMERCE  
Patent and Trademark Office

## SEARCH REQUEST FORM

Requestor's

Name:

Karen Graham Carlson

Serial

Number:

09/902772

Date:

11-6-02

Phone:

308-0034

Art Unit:

1653

9801

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

CFSE

Please search and interfere  
search Ag ID NO 1, 2, & 4.

Also nucleic acid encoding  
Ag ID NO: 2 or NO: 4.

Also 645-662 of Ag ID NO: 1,  
and especially primers.

Print out please

Thank you

Karen

nuc 1-1447

rep 4-478

rep 2-451

Point of Contact:

Barb O'Brien

Technical Information Specialist

STIC CM1 6A05 308-4291

## STAFF USE ONLY

Date completed:

11-12-02

Searcher:

P203

Terminal time:

13

Elapsed time:

over 17

CPU time:

Total time:

Number of Searches:

Number of Databases:

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG Suite

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other

Dear Examiner,

The attached search was run with the most recently released version of Compugen's search software, GenCore 5. With this update, several changes have occurred in the results of FrameSearches (protein query sequence vs nucleic acid databases or nucleic acid query sequence vs protein databases).

**In reference to FrameSearches:**

- The output format has been improved so that it more closely resembles the format for standard search output.
- Calculation of Percent Similarity has been changed for FrameSearches. The new method of calculation is more similar to the method used in NCBI's BLAST algorithm. The same results are found in the same order using GenCore 5 and the previous version of GenCore, but Percent Similarities are lower in GenCore 5 results.

- The formula for % similarity calculation is:

$$100 * \frac{\text{matches} + \text{conservative substitutions}}{\text{alignment\_length}}$$

where "matches" is the number of identical matches and "conservative substitutions" is the number of non-identical positive matches.

- GenCore 4.5 considers the match Thr vs GCT (Ala) to be a similarity since BLOSUM62 gives score of 0 to this match. It is marked by ':::' in the alignment:

```
Qy      46 AspSerThrAspAla.Met..Gly 52
          |||||:::  ||| :::  |||
Db      605 GATTCCGCTGCTGCTAATTTGGC 628
```

GenCore 5 requires a positive score to consider a non-identical match a similarity, therefore the same 'match' is not emphasized in the new alignment:

```
Qy      46 AspSerThrAspAla.Met..Gly 52
          |||||  ||| :::  |||
Db      605 GATTCCGCTGCTGCTAATTTGGC 628
```

If you have any questions, please feel free to contact one of the searchers in Biotech/Chem Library.